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RAW SEQUENCE LISTING                    DATE: 12/06/2001
PATENT APPLICATION:  US/09/837,751      TIME: 10:40:04

Input Set : A:\45-00.app
Output Set: N:\CRF3\12062001\I837751.raw
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 3 <110> APPLICANT: Green, Allan
 4          Singh, Surinder
 5          Liu, Qing
 7 <120> TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
 9 <130> FILE REFERENCE: 45-00
11 <140> CURRENT APPLICATION NUMBER: 09/837,751
12 <141> CURRENT FILING DATE: 2001-04-18
14 <150> PRIOR APPLICATION NUMBER: US 60/198,124
15 <151> PRIOR FILING DATE: 2000-04-18
17 <160> NUMBER OF SEQ ID NOS: 35
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1493
23 <212> TYPE: DNA
24 <213> ORGANISM: Gossypium sp.
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (13)..(1200)
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33                 1               5                  10
35 aag ctc cct tgc ttt gct ctt cca cca aag gcc acc ctt aga tct ccc  99
36 Lys Leu Pro Cys Phe Ala Leu Pro Pro Lys Ala Thr Leu Arg Ser Pro
37     15              20               25
39 aag ttt tcc atg atc tcc acc att cct tct ggc tcc aaa gag gtt ggg  147
40 Lys Phe Ser Met Ile Ser Thr Ile Pro Ser Gly Ser Lys Glu Val Gly
41  30                  35                40                     45
43 aat ctg aaa aag cct ttc acg cct cca aag gag gtg cct gtt cag atc  195
44 Asn Leu Lys Lys Pro Phe Thr Pro Pro Lys Glu Val Pro Val Gln Ile
45              50               55               60
47 acc cac tcc atg ccg cct cac aag att gag atc ttt aaa tct ttg gag  243
48 Thr His Ser Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Glu
49              65               70               75
51 ggc tgg gct gag aac aac att ctg act cac ctc aaa cca gtt gag aaa  291
52 Gly Trp Ala Glu Asn Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys
53          80               85               90
55 tgt tgg caa ccc gcc gac ttt ctt cca gat cct aat tct gat gga ttt  339
56 Cys Trp Gln Pro Ala Asp Phe Leu Pro Asp Pro Asn Ser Asp Gly Phe
57          95               100              105
59 cat gag caa gtc aaa gag ctt agg gaa agg gca aag gag atc cca gat  387
60 His Glu Gln Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp
61 110              115              120                      125
63 gat tac ttt gta gtt ttg gtt ggt gat atg atc acc gag gaa gcc ctt  435
64 Asp Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu
65              130              135              140
67 tca act tat caa aca atg ctt aat acc ttg gat gga act cgt gat gag  483
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68 Ser Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Thr Arg Asp Glu
69             145             150                 155
71 aca ggt gct agc ctt acc cct tgg gcc att tgg acc agg gct tgg act   531
72 Thr Gly Ala Ser Leu Thr Pro Trp Ala Ile Trp Thr Arg Ala Trp Thr
73             160             165                 170
75 gct gaa gaa aac agg cat ggt gat ctg ctt aat aag tat ctc tac ttg   579
76 Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu
77     175             180             185
79 tct ggg aga gtg gac atg agg caa att gag agg aca atc cag tac ttg   627
80 Ser Gly Arg Val Asp Met Arg Gln Ile Glu Arg Thr Ile Gln Tyr Leu
81 190             195             200                 205
83 att gga tcg gga atg gat cct cat aca gag aat agt cct tac cga gga   675
84 Ile Gly Ser Gly Met Asp Pro His Thr Glu Asn Ser Pro Tyr Arg Gly
85             210             215                 220
87 ttc ata tat act tcg ttc caa gaa agg gca act ttt att tcc cat ggg   723
88 Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly
89             225             230                 235
91 aat aca ggc agg ctg gct aag gag tat ggg gat att aac ttg gct caa   771
92 Asn Thr Gly Arg Leu Ala Lys Glu Tyr Gly Asp Ile Asn Leu Ala Gln
93             240             245             250
95 att tgt ggt agc att gcc tca gat gag aag cgc cac gag aca gcc tat   819
96 Ile Cys Gly Ser Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr
97     255             260             265
99 acc aaa atc gtt gaa aag ctg ttt gag att gat cct gat gaa aca gtc   867
100 Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Glu Thr Val
101 270             275             280                 285
103 ctg gca ttt gct gac atg atg aag aag aaa atc gcc atg ccg gct gag   915
104 Leu Ala Phe Ala Asp Met Met Lys Lys Lys Ile Ala Met Pro Ala Glu
105             290             295             300
107 ttc atc tat gat ggc aga gat tat aac tta ttt gac cac tac tca gct   963
108 Phe Ile Tyr Asp Gly Arg Asp Tyr Asn Leu Phe Asp His Tyr Ser Ala
109             305             310             315
111 gtt gcc caa aga atc ggg gtt tac act gct aag gac tat gtt gat ata   1011
112 Val Ala Gln Arg Ile Gly Val Tyr Thr Ala Lys Asp Tyr Val Asp Ile
113             320             325             330
115 gta gag cac ctg gtg gat cga tgg aag gtg aag gag cta gct ggg ctt   1059
116 Val Glu His Leu Val Asp Arg Trp Lys Val Lys Glu Leu Ala Gly Leu
117     335             340             345
119 tca gcc gag ggg cgt aaa gct cag gac tac ttg tgt tca ctt cct tcg   1107
120 Ser Ala Glu Gly Arg Lys Ala Gln Asp Tyr Leu Cys Ser Leu Pro Ser
121 350             355             360                 365
123 aga att aga agg tta gag gag aga gcg caa gaa aag gcc aag gaa gca   1155
124 Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Glu Lys Ala Lys Glu Ala
125             370             375             380
127 ccc agt gtc cca ttc agt tgg ata ttt gat aga gaa gtg aaa ctt   1200
128 Pro Ser Val Pro Phe Ser Trp Ile Phe Asp Arg Glu Val Lys Leu
129             385             390             395
131 taggtcatga aatacagtta agactcctgc aatgcatttg aggaaacaaa cacgaagaag 1260
133 aattgcgtgg ctttggttag ggtagcacat gttttctgga tgtgttgtgt ccttaaaaaa 1320
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135 taatgccgat agcggcagct gtgatagttt tagatgtttg ttttcataat gtctgttata 1380
137 tcgttgtacg agtagtatgt gttgtttttg ttgaaacaat cttcatatct tagtgataaa 1440
139 tgataatgct gtgtagtcat agtttttagt ttgcaataaa aaaaaaaaa aaa          1493
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 396
144 <212> TYPE: PRT
145 <213> ORGANISM: Gossypium sp.
147 <400> SEQUENCE: 2
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151 Cys Phe Ala Leu Pro Pro Lys Ala Thr Leu Arg Ser Pro Lys Phe Ser
152             20                  25                  30
154 Met Ile Ser Thr Ile Pro Ser Gly Ser Lys Glu Val Gly Asn Leu Lys
155             35                  40                  45
157 Lys Pro Phe Thr Pro Pro Lys Glu Val Pro Val Gln Ile Thr His Ser
158         50                  55                  60
160 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Glu Gly Trp Ala
161  65                  70                  75                  80
163 Glu Asn Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln
164                 85                  90                  95
166 Pro Ala Asp Phe Leu Pro Asp Pro Asn Ser Asp Gly Phe His Glu Gln
167             100                 105                 110
169 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
170         115                 120                 125
172 Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Ser Thr Tyr
173     130                 135                 140
175 Gln Thr Met Leu Asn Thr Leu Asp Gly Thr Arg Asp Glu Thr Gly Ala
176 145                 150                 155                 160
178 Ser Leu Thr Pro Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu
179                 165                 170                 175
181 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg
182             180                 185                 190
184 Val Asp Met Arg Gln Ile Glu Arg Thr Ile Gln Tyr Leu Ile Gly Ser
185         195                 200                 205
187 Gly Met Asp Pro His Thr Glu Asn Ser Pro Tyr Arg Gly Phe Ile Tyr
188     210                 215                 220
190 Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Gly
191 225                 230                 235                 240
193 Arg Leu Ala Lys Glu Tyr Gly Asp Ile Asn Leu Ala Gln Ile Cys Gly
194             245                 250                 255
196 Ser Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
197             260                 265                 270
199 Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Glu Thr Val Leu Ala Phe
200         275                 280                 285
202 Ala Asp Met Met Lys Lys Lys Ile Ala Met Pro Ala Glu Phe Ile Tyr
203     290                 295                 300
205 Asp Gly Arg Asp Tyr Asn Leu Phe Asp His Tyr Ser Ala Val Ala Gln
206 305                 310                 315                 320
208 Arg Ile Gly Val Tyr Thr Ala Lys Asp Tyr Val Asp Ile Val Glu His
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209                 325              330              335
211 Leu Val Asp Arg Trp Lys Val Lys Glu Leu Ala Gly Leu Ser Ala Glu
212             340              345              350
214 Gly Arg Lys Ala Gln Asp Tyr Leu Cys Ser Leu Pro Ser Arg Ile Arg
215         355              360              365
217 Arg Leu Glu Glu Arg Ala Gln Glu Lys Ala Lys Glu Ala Pro Ser Val
218     370              375              380
220 Pro Phe Ser Trp Ile Phe Asp Arg Glu Val Lys Leu
221 385              390              395
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 1411
226 <212> TYPE: DNA
227 <213> ORGANISM: Gossypium sp.
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (79)..(1233)
233 <400> SEQUENCE: 3
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236 ttctttaaag ccagcaaa atg ggt gcc ggt ggt agg atg cca att gac ggt   111
237                      Met Gly Ala Gly Gly Arg Met Pro Ile Asp Gly
238                       1               5                  10
240 ata aag gag gaa aat cga ggc tcg gtc aat cga gtt ccg atc gag aag   159
241 Ile Lys Glu Glu Asn Arg Gly Ser Val Asn Arg Val Pro Ile Glu Lys
242             15               20                  25
244 cct ccg ttt acg ctc ggt cag atc aag caa gcc att ccg ccc cac tgt   207
245 Pro Pro Phe Thr Leu Gly Gln Ile Lys Gln Ala Ile Pro Pro His Cys
246         30               35                  40
248 ttt cgc cgc tcc ctc ctt cga tcc ttc tcc tac gtg gtc cat gac cta   255
249 Phe Arg Arg Ser Leu Leu Arg Ser Phe Ser Tyr Val Val His Asp Leu
250     45               50                  55
252 tgc tta gcc tct ttc ttt tac tac att gca aca tca tat ttt cac ttt   303
253 Cys Leu Ala Ser Phe Phe Tyr Tyr Ile Ala Thr Ser Tyr Phe His Phe
254 60               65                  70                  75
256 ctc cca caa ccc ttt tcc tac att gct tgg cct gtc tat tgg gtt ctc   351
257 Leu Pro Gln Pro Phe Ser Tyr Ile Ala Trp Pro Val Tyr Trp Val Leu
258             80               85                  90
260 caa ggt tgc atc ctc acc ggt gtt tgg gtc atc gca cac gag tgg ggt   399
261 Gln Gly Cys Ile Leu Thr Gly Val Trp Val Ile Ala His Glu Trp Gly
262         95               100                 105
264 cac cac gct ttc aga gac tac caa tgg gtt gac gac acc gtc ggg ttg   447
265 His His Ala Phe Arg Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu
266         110              115                 120
268 atc ctt cat tcc gcc ctt tta gtc ccg tac ttc tcg tgg aaa atc agt   495
269 Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser
270     125              130                 135
272 cac cgc cgt cac cac tcg aac acc ggt tcc atg gag cgt gac gaa gta   543
273 His Arg Arg His His Ser Asn Thr Gly Ser Met Glu Arg Asp Glu Val
274 140              145                 150                 155
276 ttc gtg ccc aaa ccc aag tct aaa tta tca tgc ttt gcg aaa tac tta   591
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Input Set : A:\45-00.app
Output Set: N:\CRF3\12062001\I837751.raw

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277 Phe Val Pro Lys Pro Lys Ser Lys Leu Ser Cys Phe Ala Lys Tyr Leu
278               160              165              170
280 aac aat cca ccc ggt cga gtt cta tct ctt gta gtc aca ttg act ctt    639
281 Asn Asn Pro Pro Gly Arg Val Leu Ser Leu Val Val Thr Leu Thr Leu
282               175              180              185
284 ggt tgg cct atg tac tta gcc ttc aac gtt tcg ggt cga tac tat gat    687
285 Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Tyr Tyr Asp
286               190              195              200
288 cga tta gct tcc cac tat aac cct tat ggc ccc att tac tcc gat cgc    735
289 Arg Leu Ala Ser His Tyr Asn Pro Tyr Gly Pro Ile Tyr Ser Asp Arg
290       205              210              215
292 gag agg cta caa gtt tac atc tcc gat act ggt ata ttt gcg gta att    783
293 Glu Arg Leu Gln Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile
294 220              225              230              235
296 tat gta ctt tat aag att gct gca aca aaa ggg ctg gct tgg ctt tta    831
297 Tyr Val Leu Tyr Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu
298               240              245              250
300 tgc act tat ggg gtg cct cta ctt att gtg aat gcc ttc ctt gtg ttg    879
301 Cys Thr Tyr Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu
302               255              260              265
304 atc acc tac ttg caa cat act cac tcg gca ttg ccg cat tat gac tcg    927
305 Ile Thr Tyr Leu Gln His Thr His Ser Ala Leu Pro His Tyr Asp Ser
306               270              275              280
308 tcc gaa tgg gat tgg ttg cga gga gca ttg tcg acg atg gat cga gat    975
309 Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ser Thr Met Asp Arg Asp
310       285              290              295
312 ttc ggg gtg ttg aac aaa gtg ttc cat aac atc acc gat acg cat gtt   1023
313 Phe Gly Val Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val
314 300              305              310              315
316 gct cat cac ctc ttc tca acg atg cca cat tat cat gca atg gag gcc   1071
317 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
318               320              325              330
320 act aaa gca atc aaa cca ata ctc ggc aag tat tat cct ttc gac ggg   1119
321 Thr Lys Ala Ile Lys Pro Ile Leu Gly Lys Tyr Tyr Pro Phe Asp Gly
322               335              340              345
324 aca ccg att tac aag gca atg tgg agg gag gca aaa gag tgc ctt tac   1167
325 Thr Pro Ile Tyr Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr
326               350              355              360
328 gtt gag cct gac gtt ggt ggt ggt ggt ggt ggt agc aaa ggt gtt ttt   1215
329 Val Glu Pro Asp Val Gly Gly Gly Gly Gly Gly Ser Lys Gly Val Phe
330       365              370              375
332 tgg tat cgt aac aag ttc taaagaccga ccaactgcct gatagctggc         1263
333 Trp Tyr Arg Asn Lys Phe
334 380              385
336 cggcgaaatc aacgtaaaac gtacttatta gactagtgtt aactagggaa gttaataatt 1323
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340 aaactatatg gtagaaaaaa aaaaaaaa                                    1411
343 <210> SEQ ID NO: 4
344 <211> LENGTH: 385
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VERIFICATION SUMMARY　　　　　　DATE: 12/06/2001
PATENT APPLICATION:　**US/09/837,751**　　TIME: 10:40:05

Input Set : **A:\45-00.app**
Output Set: **N:\CRF3\12062001\I837751.raw**

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L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30